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## SEQUENCE LISTING

<110> Government of the United States as represented by the Secretary,  
Department of Health and Human Services, c/o Centers for Disease  
Control and Prevention

Carlone, George M.  
Ades, Edwin W.  
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Tharpe, Jean A.  
Zeiler, Joan L.  
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<120> Epitope Peptides Immunogenic Against  
Streptococcus Pneumoniae

<130> 14114.0343U2

<140> 09/623,038

<141> 2000-11-27

<150> PCT/US99/04326

<151> 1999-02-26

<150> 60/076,565

<151> 1998-03-02

<160> 8

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1330

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence; Note =  
synthetic construct

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atatttgaaa ctgaaaaata aacatttggt aaaataaggg gcaaagccct aataaattgg	180
aggatcta atg aaa aaa tta ggt aca tta ctc gtt ctc ttt ctt tct gca	230
Met Lys Lys Leu Gly Thr Leu Leu Val Leu Phe Leu Ser Ala	
1 5 10	

atc att ctt gta gca tgt gct agc gga aaa aaa gat aca act tct ggt	278
Ile Ile Leu Val Ala Cys Ala Ser Gly Lys Lys Asp Thr Thr Ser Gly	
15 20 25 30	

caa aaa cta aaa gtt gtt gct aca aac tca atc atc gct gat att act 326  
 Gln Lys Leu Lys Val Val Ala Thr Asn Ser Ile Ile Ala Asp Ile Thr  
 35 40 45

aaa aat att gct ggt gac aaa att gac ctt cat agt atc gtt ccg att 374  
 Lys Asn Ile Ala Gly Asp Lys Ile Asp Leu His Ser Ile Val Pro Ile  
 50 55 60

ggg caa gac cca cac gaa tac gaa cca ctt cct gaa gac gtt aag aaa 422  
 Gly Gln Asp Pro His Glu Tyr Glu Pro Leu Pro Glu Asp Val Lys Lys  
 65 70 75

act tct gag gct gat ttg att ttc tat aac ggt atc aac ctt gaa aca 470  
 Thr Ser Glu Ala Asp Leu Ile Phe Tyr Asn Gly Ile Asn Leu Glu Thr  
 80 85 90

ggt ggc aat gct tgg ttt aca aaa ttg gta gaa aat gcc aag aaa act 518  
 Gly Gly Asn Ala Trp Phe Thr Lys Leu Val Glu Asn Ala Lys Lys Thr  
 95 100 105 110

gaa aac aaa gac tac ttc gca gtc agc gac ggc gtt gat gtt atc tac 566  
 Glu Asn Lys Asp Tyr Phe Ala Val Ser Asp Gly Val Asp Val Ile Tyr  
 115 120 125

ctt gaa ggt caa aat gaa aaa gga aaa gaa gac cca cac gct tgg ctt 614  
 Leu Glu Gly Gln Asn Glu Lys Gly Lys Glu Asp Pro His Ala Trp Leu  
 130 135 140

aac ctt gaa aac ggt att att ttt gct aaa aat atc gcc aaa caa ttg 662  
 Asn Leu Glu Asn Gly Ile Ile Phe Ala Lys Asn Ile Ala Lys Gln Leu  
 145 150 155

agc gcc aaa gac cct aac aat aaa gaa ttc tat gaa aaa aat ctc aaa 710  
 Ser Ala Lys Asp Pro Asn Asn Lys Glu Phe Tyr Glu Lys Asn Leu Lys  
 160 165 170

gaa tat act gat aag tta gac aaa ctt gat aaa gaa agt aag gat aaa 758  
 Glu Tyr Thr Asp Lys Leu Asp Lys Leu Asp Lys Glu Ser Lys Asp Lys  
 175 180 185 190

ttt aat aag atc cct gct gaa aag aaa ctc att gta acc agc gaa gga 806  
 Phe Asn Lys Ile Pro Ala Glu Lys Lys Leu Ile Val Thr Ser Glu Gly  
 195 200 205

gca ttc aaa tac ttc tct aaa gcc tat ggt gtc cca agt gcc tac atc 854  
 Ala Phe Lys Tyr Phe Ser Lys Ala Tyr Gly Val Pro Ser Ala Tyr Ile  
 210 215 220

tgg gaa atc aat act gaa gaa gaa gga act cct gaa caa atc aag acc 902  
 Trp Glu Ile Asn Thr Glu Glu Glu Gly Thr Pro Glu Gln Ile Lys Thr  
 225 230 235

ttg gtt gaa aaa ctt cgc caa aca aaa gtt cca tca ctc ttt gta gaa 950  
 Leu Val Glu Lys Leu Arg Gln Thr Lys Val Pro Ser Leu Phe Val Glu  
 240 245 250

tca agt gtg gat gac cgt cca atg aaa act gtt tct caa gac aca aac 998  
 Ser Ser Val Asp Asp Arg Pro Met Lys Thr Val Ser Gln Asp Thr Asn  
 255 260 265 270

atc cca atc tac gca caa atc ttt act gac tct atc gca gaa caa ggt 1046  
 Ile Pro Ile Tyr Ala Gln Ile Phe Thr Asp Ser Ile Ala Glu Gln Gly  
 275 280 285

aaa gaa ggc gac agc tac tac agc atg atg aaa tac aac ctt gac aag 1094  
 Lys Glu Gly Asp Ser Tyr Tyr Ser Met Met Lys Tyr Asn Leu Asp Lys  
 290 295 300

att gct gaa gga ttg gca aaa taagcctctg aaaaacgtca ttctcatgtg 1145  
 Ile Ala Glu Gly Leu Ala Lys  
 305

agctggcggtt ttttctatgc ccacatttcc ggtcaaatca ttggaaaatt ctgactgttt 1205  
 cagataacaat ggaagaaaaa agattggagt atcctatggt aacttttctc ggaaatcctg 1265  
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 20 25 30  
 Leu Lys Val Val Ala Thr Asn Ser Ile Ile Ala Asp Ile Thr Lys Asn  
 35 40 45  
 Ile Ala Gly Asp Lys Ile Asp Leu His Ser Ile Val Pro Ile Gly Gln  
 50 55 60  
 Asp Pro His Glu Tyr Glu Pro Leu Pro Glu Asp Val Lys Lys Thr Ser  
 65 70 75 80  
 Glu Ala Asp Leu Ile Phe Tyr Asn Gly Ile Asn Leu Glu Thr Gly Gly  
 85 90 95  
 Asn Ala Trp Phe Thr Lys Leu Val Glu Asn Ala Lys Lys Thr Glu Asn  
 100 105 110  
 Lys Asp Tyr Phe Ala Val Ser Asp Gly Val Asp Val Ile Tyr Leu Glu  
 115 120 125  
 Gly Gln Asn Glu Lys Gly Lys Glu Asp Pro His Ala Trp Leu Asn Leu  
 130 135 140  
 Glu Asn Gly Ile Ile Phe Ala Lys Asn Ile Ala Lys Gln Leu Ser Ala  
 145 150 155 160  
 Lys Asp Pro Asn Asn Lys Glu Phe Tyr Glu Lys Asn Leu Lys Glu Tyr  
 165 170 175

Thr Asp Lys Leu Asp Lys Leu Asp Lys Glu Ser Lys Asp Lys Phe Asn  
 180 185 190  
 Lys Ile Pro Ala Glu Lys Lys Leu Ile Val Thr Ser Glu Gly Ala Phe  
 195 200 205  
 Lys Tyr Phe Ser Lys Ala Tyr Gly Val Pro Ser Ala Tyr Ile Trp Glu  
 210 215 220  
 Ile Asn Thr Glu Glu Glu Gly Thr Pro Glu Gln Ile Lys Thr Leu Val  
 225 230 235 240  
 Glu Lys Leu Arg Gln Thr Lys Val Pro Ser Leu Phe Val Glu Ser Ser  
 245 250 255  
 Val Asp Asp Arg Pro Met Lys Thr Val Ser Gln Asp Thr Asn Ile Pro  
 260 265 270  
 Ile Tyr Ala Gln Ile Phe Thr Asp Ser Ile Ala Glu Gln Gly Lys Glu  
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 Gly Asp Ser Tyr Tyr Ser Met Met Lys Tyr Asn Leu Asp Lys Ile Ala  
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<210> 4  
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21

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<210> 8  
<211> 15  
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<400> 8  
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